

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 23, 2002, 14:39:08 ; Search time 16.16 seconds  
(without alignments)  
1111.925 Million cell updates/sec

Title: US-09-811-118-1

Perfect score: 187

Sequence: 1 MVAATVAAAMLILMAACAQ.....VRLQITVALVKLILKREDL 187

Scoring table: OLIGO

Searched: 283138 seqs, 96089334 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR\_71.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	7.0	167	2	T14262 glutathione peroxi
2	11	5.9	169	2	S75885 glutathione peroxi
3	10	5.3	160	2	F87463 glutathione peroxi
4	10	5.3	163	2	T23936 hypothetical prote
5	10	5.3	236	2	T06462 glutathione peroxi
6	9	4.8	116	2	S56693 glutathione peroxi
7	9	4.8	134	2	S68899 glutathione peroxi
8	9	4.8	163	2	T21418 hypothetical prote
9	9	4.8	167	1	S33618 glutathione peroxi
10	9	4.8	169	1	S20501 probable glutathio
11	9	4.8	169	2	T04207 phospholipid-hydro
12	9	4.8	170	1	JN0608 phospholipid-hydro
13	9	4.8	170	1	JC4332 phospholipid-hydro
14	9	4.8	171	2	JC5619 phospholipid-hydro
15	9	4.8	173	2	T48097 glutathione peroxi
16	9	4.8	180	2	T12633 glutathione peroxi
17	9	4.8	192	2	C96660 protein FK1.16 l
18	9	4.8	206	2	A84865 probable glutathio
19	9	4.8	230	2	T06309 glutathione peroxi
20	9	4.8	236	2	A84644 glutathione peroxi
21	9	4.8	242	1	S71250 probable glutathio
22	8	4.3	169	2	D84722 glutathione peroxi
23	8	4.3	171	2	A84924 probable glutathio
24	8	4.3	193	2	T16662 hypothetical prote
25	8	4.3	449	2	C82688 tryptophan synthet
26	8	4.3	508	2	E81875 threonine dehydrat
27	8	4.3	508	2	A81147 threonine dehydrat
28	8	4.3	769	2	S35458 SNF2 protein homol
29	8	4.3	1531	2	T42218 slit-1 protein hom

30	7	3.7	96	2	S65794 glutathione peroxi
31	7	3.7	122	2	S05317 glutathione peroxi
32	7	3.7	122	2	H83110 50S ribosomal prot
33	7	3.7	126	2	D83475 hypothetical prote
34	7	3.7	155	2	S56258 hypothetical prote
35	7	3.7	158	2	T43376 glutathione peroxi
36	7	3.7	158	2	D89905 glutathione peroxi
37	7	3.7	160	2	F83541 probable glutathio
38	7	3.7	161	2	H83292 probable glutathio
39	7	3.7	162	2	S45121 probable glutathio
40	7	3.7	162	2	T09638 probable glutathio
41	7	3.7	163	1	S48499 glutathione peroxi
42	7	3.7	167	2	T44271 glutathione peroxi
43	7	3.7	174	2	B83673 hypothetical prote
44	7	3.7	183	1	ORECBE vitamin B12 transp
45	7	3.7	183	2	A98931 vitamin B12 transp

#### ALIGNMENTS

RESULT 1  
T14262  
glutathione peroxidase (EC 1.11.1.9) - common sunflower  
C:Species: Helianthus annuus (common sunflower)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T14262  
R.Roeckel-Drevet, P.; Gagne, G.; Tourville de Labrouhe, D.; Dufaire, J.P.; Nicolas, Physiol. Plantarum 103, 385-394, 1998  
A:Title: Molecular characterization, organ distribution and stress-mediated induction  
A:Reference number: 217562  
A:Accession: T14262  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-167 <ROE>  
A:Cross-References: EMBL:Y14429  
C:Genetics:  
A:Gene: GPxha-1  
C:Function:  
A:Description: catalyzes reduction of hydroperoxides by glutathione, thus protecting  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase

Query Match 7.0%: Score 13; DB 2; Length 167;  
Best Local Similarity 100.0%: Pred. No. 1.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 LAFCNQGQGP 94  
Db 66 LAFCNQGQGP 78

RESULT 2  
S75885  
glutathione peroxidase homolog sir1171 - Synecocystis sp. (strain PCC 6803)  
N:Alternate names: protein sir1171  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S75885  
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys  
s.  
A:Reference number: S74322; MUID:97061201  
A:Accession: S75885  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-169 <KAN>  
A:Cross-References: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BA18344.1; PID:g165  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

## C:Superfamily: glutathione peroxidase

Query Match 5.9%; Score 11; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 FPCNOFGOEP 94  
|||||  
DB 67 FPCNOFGOEP 77

## RESULT 3

F87463  
glutathione peroxidase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: F87463  
R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MIMD:21173698; PMID:11259647  
A:Accession: F87463

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-160 <STO>  
A:Cross-references: GB:AE005673; NID:gl3423148; PIDN:AAK23706.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CCI1730  
C:Superfamily: glutathione peroxidase

Query Match 5.3%; Score 10; DB 2; Length 160;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VIAFPCNOFG 90  
|||||  
DB 60 VIAFPCNOFG 69

## RESULT 4

T23936  
hypothetical protein R05H10.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T23936  
R:McMurray, A.  
submitted to the EMBL Data Library, November 1996

A:Reference number: Z19820  
A:Accession: T23936  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-163 <MTL>  
A:Cross-references: EMBL:Z83119; PIDN:CAB05581.1; GSPDB:GN00020; CESP:R05H10.5  
A:Experimental source: clone R05H10  
C:Genetics:  
A:Gene: CESP:R05H10.5  
A:Map position: 2  
A:Introns: 23/2; 52/2  
C:Superfamily: glutathione peroxidase

Query Match 5.3%; Score 10; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VIAFPCNOFG 90  
|||||  
DB 60 VIAFPCNOFG 69

## RESULT 5

T06462  
glutathione peroxidase (EC 1.11.1.9) precursor - garden pea

N:Alternate names: phospholipid glutathione peroxidase  
C:Species: Pisum sativum (garden pea)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 21-Jul-2000  
C:Accession: T06462  
R:Multineux, P.M.; Karpinski, S.; Jimenez, A.; Cleary, S.P.; Robinson, C.; Creissen,  
Plant J. 13, 375-379, 1998  
A:Title: Identification of cDNAs encoding plastid-targeted glutathione peroxidase.  
A:Reference number: Z15696; MIMD:98345965  
A:Accession: T06462

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <MUL>  
A:Cross-references: EMBL:AJ000508; NID:g2632108; PIDN:CAA04142.1; PID:g2632109  
A:Experimental source: cv. Blüte  
C:Genetics:  
A:Map position: 1  
A:Genome: nuclear  
C:Superfamily: glutathione peroxidase  
C:Keywords: chloroplast; oxidoreductase; selenocysteine

Query Match 5.3%; Score 10; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VIAFPCNOFG 90  
|||||  
DB 135 VIAFPCNOFG 144

## RESULT 6

S56693  
glutathione peroxidase (EC 1.11.1.9) - wild oat (fragment)

C:Species: Avena fatua (wild oat)  
C:Date: 10-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 11-Jun-1999  
C:Accession: S56693  
R:Johnson, R.R.; Cranston, H.J.; Chaverra, M.E.; Dyer, W.E.  
Plant Mol. Biol. 28, 113-122, 1995  
A:Title: Characterization of cDNA clones for differentially expressed genes in embryo  
A:Reference number: S56690; MIMD:95306780  
A:Accession: S56693

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-116 <JON>  
A:Cross-references: EMBL:U20000; NID:g726477; PIDN:AAV6742.1; PID:g726478  
A:Experimental source: clone AFN3  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90  
|||||  
DB 15 LAFPCNOFG 23

## RESULT 7

S68899

glutathione peroxidase (EC 1.11.1.9) - fluke (Schistosoma mansoni) (fragments)

C:Species: Schistosoma mansoni  
C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 12-Dec-1997  
C:Accession: S68899  
R:Majorino, M.; Roche, C.; Kless, M.; Koenig, K.; Gawlik, D.; Mattes, M.; Naldini, E.  
Eur. J. Biochem. 238, 838-844, 1996  
A:Title: A selenium-containing phospholipid-hydroperoxide glutathione peroxidase in S

A:Reference number: S68899; MUID:96300252  
A:Accession: S68899  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11,12-25;26-28;29-67;68-82;83-134 <MAT>  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase; selenium; selenocysteine

Query Match 4.8%; Score 9; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFCNCFG 90  
|||||  
DB 48 LAFCNCFG 56

## RESULT 8

T21418  
hypothetical protein F26E4.12 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T21418  
R:Lightning, J.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19419  
A:Accession: T21418  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-163 <WIL>  
A:Cross-references: EMBL:Z81070; PIDN:CA803004.1; GSPDB:GN00019; CESP:F26E4.12  
A:Experimental source: clone F26E4  
C:Genetics:  
A:Gene: CESP:F26E4.12  
A:Map position: 1  
A:Introns: 23/2; 52/2  
C:Superfamily: glutathione peroxidase

Query Match 4.8%; Score 9; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 VLAFPCNOF 89  
|||||  
DB 60 VLAFPCNOF 68

## RESULT 9

S33618  
glutathione peroxidase (EC 1.11.1.9) - sweet orange  
N:Alternate names: salt-associated protein csaa  
C:Species: Citrus sinensis (sweet orange)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S33618; S36373  
R:Holland, D.; Ben-Hayim, G.; Faltin, Z.; Camolin, L.; Strosberg, A.D.; Eshdat, Y.  
Plant Mol. Biol. 21, 923-927, 1993  
A:Title: Molecular characterization of salt-stress-associated protein in citrus: protein  
A:Reference number: S33618; MUID:93222490  
A:Accession: S33618  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-167 <HOZ>  
A:Cross-references: EMBL:X66377  
A>Note: part of this sequence was confirmed by protein sequencing  
R:Holland, D.  
submitted to the EMBL Data Library, May 1992  
A:Reference number: S36373  
A:Accession: S36373  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-52, 0', 54-167 <HOZ>

A:Cross-references: EMBL:X66377; NID:g296357; PIDN:CAA47018.1; PID:g296358  
C:Genetics:  
A:Gene: csaa  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase; selenocysteine  
F:41/Modified site: selenocysteine #status predicted

Query Match 4.8%; Score 9; DB 1; Length 167;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFCNCFG 90  
|||||  
DB 66 LAFCNCFG 74

## RESULT 10

S20501  
probable glutathione peroxidase (EC 1.11.1.9) - wood tobacco  
C:Species: Nicotiana glauca (wood tobacco)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S20501  
R:Crizqui, M.C.; Jamet, E.; Parmentier, Y.; Marbach, J.; Durr, A.; Fleck, J.  
Plant Mol. Biol. 18, 623-627, 1992  
A:Title: Isolation and characterization of a plant cDNA showing homology to animal gl  
A:Reference number: S20501; MUID:92163033  
A:Accession: S20501  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-169 <CR1>  
A:Cross-references: EMBL:X60219; NID:g19738; PIDN:CAA42780.1; PID:g19739  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFCNCFG 90  
|||||  
DB 68 LAFCNCFG 76

## RESULT 11

T04207  
phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - Arabidopsis thaliana  
N:Alternate names: protein TSC23.30  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 03-Nov-2000  
C:Accession: T04207; T52116  
R:Bevan, M.; Hilbert, H.; Brun, M.; Holzer, E.; Brandt, A.; Duesternoeft, A.; Bancro  
submitted to the Protein Sequence Database, March 1999  
A:Reference number: Z15261  
A:Accession: T04207  
A:Molecule type: DNA  
A:Residues: 1-169 <BEV>  
A:Cross-references: EMBL:AL049500  
A:Experimental source: cultivar Columbia; BAC clone TSC23  
R:Bilodeau, P.  
submitted to the EMBL Data Library, October 1997  
A:Reference number: Z25963  
A:Accession: T52116  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-169 <BIT>  
A:Cross-references: EMBL:AF030132; PIDN:AAC09173.1  
C:Genetics:  
A:Map position: 4  
A:Introns: 16/3; 42/2; 63/1; 102/3; 158/3  
A>Note: TSC23.30  
C:Superfamily: glutathione peroxidase

## C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90  
|||||  
DB 67 LAFPCNOFG 75

## RESULT 12

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JN0608; A53395; A54649  
R:Sunde, R.A.; Dyer, J.A.; Moran, T.V.; Evenson, J.K.; Sugimoto, M.  
Biochem. Biophys. Res. Commun. 193, 905-911, 1993  
A:Title: Phospholipid hydroperoxide glutathione peroxidase: full-length pig blastocyst  
A:Reference number: JN0608; MUID:93312346  
A:Accession: JN0608  
A:Molecule type: mRNA  
A:Residues: 1-170 <SUN>  
A:Cross-references: GB:LI2743; NID:9294224; PIDN:AAA31099.1; PID:9294226  
A:Experimental source: blastocyst  
R:Brigelius-Flohe, R.; Annam, K.D.; Bloeker, H.; Gross, G.; Kiess, M.; Kloeppel, K.D.;  
J. Biol. Chem. 269, 7342-7348, 1994  
A:Title: Phospholipid-hydroperoxide glutathione peroxidase. Genomic DNA, cDNA, and deduc  
A:Reference number: A53395; MUID:94171752  
A:Accession: A53395  
A:Status: Preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-45, 'S', '47-170 <BRI>  
A:Cross-references: GB:X76008; NID:9473358; PIDN:CAA53595.1; PID:92654294; GB:X76009; NT  
R:Schuckelt, R.; Brigelius-Flohe, R.; Maiorino, M.; Roveri, A.; Reumens, J.; Strassburg  
Free Radic. Res. Commun. 14, 343-361, 1991  
A:Title: Phospholipid hydroperoxide glutathione peroxidase is a selenoenzyme distinct fr  
A:Reference number: A54649; MUID:92137773  
A:Accession: A54649  
A:Status: Preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 13-45, 47-170 <SCH>  
A:Cross-references: GB:S80257; NID:9244650; PIDN:AA21327.1; PID:9244651  
A:Experimental source: heart  
A:Note: sequence extracted from NCBJ backbone (NCBIN:80257, NCBIP:80258)  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase; selenocysteine  
F:46/Modified site: selenocysteine #status predicted

Query Match 4.8%; Score 9; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90  
|||||  
DB 71 LAFPCNOFG 79

## RESULT 13

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JC4332  
R:Imai, H.; Sumi, D.; Hanamoto, A.; Arai, M.; Sugiyama, A.; Chiba, N.; Kuchino, Y.; Nak  
J. Biochem. 118, 1061-1067, 1995  
A:Title: Molecular cloning and functional expression of a cDNA for rat phospholipid hyd  
A:Reference number: JC4332; MUID:96318522  
A:Accession: JC4332  
A:Molecule type: mRNA

## A:Residues: 1-170 &lt;IMA&gt;

A:Cross-references: EMBL:X82679; NID:91041644; PIDN:CAA57996.1; PID:91041645  
A:Experimental source: brain  
A:Comment: This enzyme is a unique enzyme in glutathione peroxidase and is a selenopr  
es. It defenses against oxidative destruction of biomembranes.  
C:Genetics:  
A:Introns: 45/3  
C:Superfamily: glutathione peroxidase  
C:Keywords: brain; oxidoreductase; phospholipid; selenocysteine  
F:46/Modified site: selenocysteine #status experimental

Query Match 4.8%; Score 9; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90  
|||||  
DB 71 LAFPCNOFG 79

## RESULT 14

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - spinach  
N:Alternate names: peroxidation-inhibiting protein  
C:Species: Spinacia oleracea (spinach)  
C:Date: 09-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Jun-2000  
C:Accession: JC5619  
R:Sugimoto, M.; Futui, S.; Suzuki, Y.  
Biosci. Biotechnol. Biochem. 61, 1379-1381, 1997  
A:Title: Molecular cloning and characterization of a cDNA encoding putative phosphol  
A:Reference number: JC5619; MUID:97446534  
A:Accession: JC5619  
A:Molecule type: mRNA  
A:Residues: 1-171 <SUC>  
A:Cross-references: DDBJ:D63425; NID:92392020; PIDN:BA22194.1; PID:92392021  
A:Comment: This enzyme catalyzes the reduction of hydroperoxides of phospholipids act  
C:Genetics:  
A:Gene: phyx  
C:Superfamily: glutathione peroxidase  
C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 171;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90  
|||||  
DB 69 LAFPCNOFG 77

## RESULT 15

glutathione peroxidase-like protein - Arabidopsis thaliana  
N:Alternate names: protein T20010.180  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 19-May-2000  
C:Accession: T48097  
R:Overmeyer, B.; Ottenwelder, B.; Duchemin, D.; Zeitler, K.; Newes, H.W.; Rudd, S.;  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 224484  
A:Accession: T48097  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-173 <OBE>  
A:Cross-references: EMBL:AL163816  
A:Experimental source: cultivar Columbia; BAC clone T20010  
C:Genetics:  
A:Map position: 3  
A:Introns: 20/3; 46/2; 67/1; 106/3; 162/3  
A:Note: T20010.180  
C:Superfamily: glutathione peroxidase

Query Match 4.8%; Score 9; DB 2; Length 173;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 VLAFCNDF 89  
|||||||  
Db 70 VLAFCNDF 78

Search completed: August 23, 2002, 14:41:16  
Job time: 128 sec

